

SEQUENCE SUBMISSION

SEQ ID NO: 1 provides primate IL-1 δ nucleotide sequence.
 SEQ ID NO: 2 provides primate IL-1 δ polypeptide sequence.
 5 SEQ ID NO: 3 provides primate IL-1 ϵ nucleotide sequence.
 SEQ ID NO: 4 provides primate IL-1 ϵ polypeptide sequence.
 SEQ ID NO: 5 provides primate IL-1 α polypeptide sequence.
 SEQ ID NO: 6 provides primate IL-1 β polypeptide sequence.
 10 SEQ ID NO: 7 provides primate IL-1RA polypeptide sequence.
 SEQ ID NO: 8 provides rodent IL-1 γ (IGIF) polypeptide sequence.
 SEQ ID NO: 9 provides primate IL-1 γ (IGIF) polypeptide sequence.
 SEQ ID NO: 10 provides rodent IL-1 ϵ polypeptide sequence.
 SEQ ID NO: 11 provides rodent IL-1 δ polypeptide sequence.
 15 SEQ ID NO: 12 provides primate IL-1R6 nucleotide sequence.
 SEQ ID NO: 13 provides primate IL-1R6 polypeptide sequence.
 SEQ ID NO: 14 provides rodent IL-1R6 nucleotide sequence.
 SEQ ID NO: 15 provides rodent IL-1R6 polypeptide sequence.

20 <110> Debets, Johannes E.M.A.
 Timans, Jacqueline C.
 Bazan, J. Fernando
 Kastelein, Robert A.

25 <120> Mammalian Cytokines; Receptors; Related Reagents and
 Methods
 <130> DX01073P

30 <140>
 <141>
 <160> 15

35 <170> PatentIn Ver. 2.1
 <210> 1
 <211> 1025
 <212> DNA
 40 <213> Unknown Organism
 <220>
 <223> Description of Unknown Organism: primate; surmised
 Homo sapiens

45 <220>
 <221> CDS
 <222> (58)..(522)

50 <400> 1
 gctcccgcca ggagaaagga acattctgag gggagtctac accctgtgga gctcaag 57
 atg gtc ctg agt ggg gcg ctg tgc ttc cga atg aag gac tcg gca ttg 105
 Met Val Leu Ser Gly Ala Leu Cys Phe Arg Met Lys Asp Ser Ala Leu
 55 1 5 10 15
 aag gtg ctt tat ctg cat aat aac cag ctt cta gct gga ggg ctg cat 153
 Lys Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly Leu His
 20 25 30

60

1073K 54052260

	gca ggg aag gtc att aaa ggt gaa gag atc agc gtg gtc ccc aat cgg	201
	Ala Gly Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn Arg	
	35 40 45	
5	tgg ctg gat gcc agc ctg tcc ccc gtc atc ctg ggt gtc cag ggt gga	249
	Trp Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly Gly	
	50 55 60	
10	agc cag tgc ctg tca tgt ggg gtg ggg cag gag ccg act cta aca cta	297
	Ser Gln Cys Leu Ser Cys Gly Val Gly Gln Glu Pro Thr Leu Thr Leu	
	65 70 75 80	
15	gag cca gtg aac atc atg gag ctc tat ctt ggt gcc aag gaa tcc aag	345
	Glu Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser Lys	
	85 90 95	
20	agc ttc acc ttc tac cgg cgg gac atg ggg ctc acc tcc agc ttc gag	393
	Ser Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe Glu	
	100 105 110	
25	tcg gct gcc tac ccg ggc tgg ttc ctg tgc acg gtg cct gaa gcc gat	441
	Ser Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Val Pro Glu Ala Asp	
	115 120 125	
30	cag cct gtc aga ctc acc cag ctt ccc gag aat ggt ggc tgg aat gcc	489
	Gln Pro Val Arg Leu Thr Gln Leu Pro Glu Asn Gly Gly Trp Asn Ala	
	130 135 140	
35	ccc atc aca gac ttc tac ttc cag cag tgt gac tagggcaacg tgccccccag	542
	Pro Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp	
	145 150 155	
40	aactccttgg gcagagccag ctcggttgag gggtgagtgg aggagacca tggcggacaa	602
	teactctctc tgctctcagg acccccacgt ctgacttagt gggcacctga ccactttgtc	662
	ttctgggttcc cagtttggat aaattctgag atttgaggct cagtccacgg tcctccccca	722
	ctggatgggtg ctactgctgt ggaaccttgt aaaaaccatg tggggtaaac tgggaataac	782
	atgaaaagat ttctgtgggg gtgggggtggg gaagtgggtgg ggaatcatte ctgcttaatg	842
	gtaactgaca agtgttaccc tgagccccgc aggccaaccc atccccagtt gaggcttata	902
45	gggtcagtag ctctccacat gaagtctgt cactcaccac tgtgcaggaa gggaagggtg	962
	tcatagagta agggatctat ggcccttggc ccagccccac cccttccctt taatcctgcc	1022
50	act	1025
	<210> 2	
	<211> 155	
	<212> PRT	
55	<213> Unknown Organism	
	<223> Description of Unknown Organism: primate; surmised Homo sapiens	
	<400> 2	
60	Met Val Leu Ser Gly Ala Leu Cys Phe Arg Met Lys Asp Ser Ala Leu	
	1 5 10 15	

	Lys	Val	Leu	Tyr	Leu	His	Asn	Asn	Gln	Leu	Leu	Ala	Gly	Gly	Leu	His	
				20					25						30		
5	Ala	Gly	Lys	Val	Ile	Lys	Gly	Glu	Glu	Ile	Ser	Val	Val	Pro	Asn	Arg	
			35					40					45				
	Trp	Leu	Asp	Ala	Ser	Leu	Ser	Pro	Val	Ile	Leu	Gly	Val	Gln	Gly	Gly	
		50					55					60					
10	Ser	Gln	Cys	Leu	Ser	Cys	Gly	Val	Gly	Gln	Glu	Pro	Thr	Leu	Thr	Leu	
	65					70					75					80	
	Glu	Pro	Val	Asn	Ile	Met	Glu	Leu	Tyr	Leu	Gly	Ala	Lys	Glu	Ser	Lys	
15					85					90					95		
	Ser	Phe	Thr	Phe	Tyr	Arg	Arg	Asp	Met	Gly	Leu	Thr	Ser	Ser	Phe	Glu	
				100					105					110			
20	Ser	Ala	Ala	Tyr	Pro	Gly	Trp	Phe	Leu	Cys	Thr	Val	Pro	Glu	Ala	Asp	
			115					120					125				
	Gln	Pro	Val	Arg	Leu	Thr	Gln	Leu	Pro	Glu	Asn	Gly	Gly	Trp	Asn	Ala	
			130				135					140					
25	Pro	Ile	Thr	Asp	Phe	Tyr	Phe	Gln	Gln	Cys	Asp						
	145					150					155						
30	<210>	3															
	<211>	1073															
	<212>	DNA															
	<213>	Unknown Organism															
35	<220>																
	<223>	Description of Unknown Organism:	primate;	surmised													
		Homo sapiens															
40	<220>																
	<221>	CDS															
	<222>	(67)..(573)															
	<400>	3															
45	ccacgattca	gtcccctgga	ctgtagataa	agaccctttc	ttgccagggtg	ctgagacaac	60										
	cacact	atg aga ggc act cca gga gac gct gat ggt gga gga agg gcc	108														
		Met Arg Gly Thr Pro Gly Asp Ala Asp Gly Gly Gly Arg Ala															
		1			5					10							
50	gtc tat caa tca atg tgt aaa cct att act ggg act att aat gat ttg	156															
	Val Tyr Gln Ser Met Cys Lys Pro Ile Thr Gly Thr Ile Asn Asp Leu																
	15				20					25						30	
55	aat cag caa gtg tgg acc ctt cag ggt cag aac ctt gtg gca gtt cca	204															
	Asn Gln Gln Val Trp Thr Leu Gln Gly Gln Asn Leu Val Ala Val Pro																
					35					40						45	
60	cga agt gac agt gtg acc cca gtc act gtt gct gtt atc aca tgc aag	252															
	Arg Ser Asp Ser Val Thr Pro Val Thr Val Ala Val Ile Thr Cys Lys																
					50					55						60	

tat cca gag gct ctt gag caa ggc aga ggg gat ccc att tat ttg gga 300
 Tyr Pro Glu Ala Leu Glu Gln Gly Arg Gly Asp Pro Ile Tyr Leu Gly
 65 70 75
 5 atc cag aat cca gaa atg tgt ttg tat tgt gag aag gtt gga gaa cag 348
 Ile Gln Asn Pro Glu Met Cys Leu Tyr Cys Glu Lys Val Gly Glu Gln
 80 85 90
 10 ccc aca ttg cag cta aaa gag cag aag atc atg gat ctg tat ggc caa 396
 Pro Thr Leu Gln Leu Lys Glu Gln Lys Ile Met Asp Leu Tyr Gly Gln
 95 100 105 110
 15 ccc gag ccc gtg aaa ccc ttc ctt ttc tac cgt gcc aag act ggt agg 444
 Pro Glu Pro Val Lys Pro Phe Leu Phe Tyr Arg Ala Lys Thr Gly Arg
 115 120 125
 20 acc tcc acc ctt gag tct gtg gcc ttc ccg gac tgg ttc att gcc tcc 492
 Thr Ser Thr Leu Glu Ser Val Ala Phe Pro Asp Trp Phe Ile Ala Ser
 130 135 140
 25 tcc aag aga gac cag ccc atc att ctg act tca gaa ctt ggg aag tca 540
 Ser Lys Arg Asp Gln Pro Ile Ile Leu Thr Ser Glu Leu Gly Lys Ser
 145 150 155
 30 tac aac act gcc ttt gaa tta aat ata aat gac tgaactcagc ctagagggtgg 593
 Tyr Asn Thr Ala Phe Glu Leu Asn Ile Asn Asp
 160 165
 35 cagcttggtc tttgtcttaa agtttctggt tcccaatgtg ttttcgtcta cattttctta 653
 gtgtcatttt cacgctggtg ctgagacagg ggcaaggctg ctgttatcat ctcattttat 713
 aatgaagaag aagcaattac ttcataagcaa ctgaagaaca ggatgtggcc tcagaagcag 773
 40 gagagctggg tgggtataagg ctgtcctctc aagctggtgc tgtgtaggcc acaaggcatc 833
 tgcatagagt actttaagac tcaaaagacca aacactgagc tttcttctag ggggtgggtat 893
 45 gaagatgctt cagagctcat gcgcgttacc cacgatggca tgactagcac agagctgac 953
 tctgtttctg ttttgcttta ttccctcttg ggatgatata atccagtctt tatatgttgc 1013
 caatatacct cattgtgtgt aatagaacct tcttagcatt aagaccttgt aaacaaaaat 1073
 <210> 4
 <211> 169
 <212> PRT
 50 <213> Unknown Organism
 <223> Description of Unknown Organism: primate; surmised
 Homo sapiens
 <400> 4
 55 Met Arg Gly Thr Pro Gly Asp Ala Asp Gly Gly Gly Arg Ala Val Tyr
 1 5 10 15
 Gln Ser Met Cys Lys Pro Ile Thr Gly Thr Ile Asn Asp Leu Asn Gln
 20 25 30
 60 Gln Val Trp Thr Leu Gln Gly Gln Asn Leu Val Ala Val Pro Arg Ser

[illegible]

Ala Gly Gly Pro Pro Ser Ile Thr Asp Phe Gln Ile Leu Glu Asn Gln
 130 135 140

5 Ala
 145

10 <210> 6
 <211> 153
 <212> PRT
 <213> Unknown Organism

15 <220>
 <223> Description of Unknown Organism: primate; surmised
 Homo sapiens

20 <400> 6
 Ala Pro Val Arg Ser Leu Asn Cys Thr Leu Arg Asp Ser Gln Gln Lys
 1 5 10 15

Ser Leu Val Met Ser Gly Pro Tyr Glu Leu Lys Ala Leu His Leu Gln
 20 25 30

25 Gly Gln Asp Met Glu Gln Gln Val Val Phe Ser Met Ser Phe Val Gln
 35 40 45

Gly Glu Glu Ser Asn Asp Lys Ile Pro Val Ala Leu Gly Leu Lys Glu
 50 55 60

30 Lys Asn Leu Tyr Leu Ser Cys Val Leu Lys Asp Asp Lys Pro Thr Leu
 65 70 75 80

35 Gln Leu Glu Ser Val Asp Pro Lys Asn Tyr Pro Lys Lys Lys Met Glu
 85 90 95

Lys Arg Phe Val Phe Asn Lys Ile Glu Ile Asn Asn Lys Leu Glu Phe
 100 105 110

40 Glu Ser Ala Gln Phe Pro Asn Trp Tyr Ile Ser Thr Ser Gln Ala Glu
 115 120 125

Asn Met Pro Val Phe Leu Gly Gly Thr Lys Gly Gly Gln Asp Ile Thr
 130 135 140

45 Asp Phe Thr Met Gln Phe Val Ser Ser
 145 150

50 <210> 7
 <211> 147
 <212> PRT
 <213> Unknown Organism

55 <220>
 <223> Description of Unknown Organism: primate; surmised
 Homo sapiens

60 <400> 7
 Lys Ser Ser Lys Met Gln Ala Phe Arg Ile Trp Asp Val Asn Gln Lys
 1 5 10 15

20250925 14:26:26

115 120 125

Asp Asp Ala Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp
130 135 140

5 Lys Ser Val Met Phe Thr Leu Thr Asn Leu His Gln Ser
145 150 155

10 <210> 9
<211> 157
<212> PRT
<213> Unknown Organism

15 <220>
<223> Description of Unknown Organism: primate; surmised
Homo sapiens

20 <400> 9
Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn Leu Asn
1 5 10 15

Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe Glu Asp
20 25 30

25 Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg Thr Ile Phe Ile
35 40 45

30 Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val Thr Ile
50 55 60

Ser Val Lys Cys Glu Lys Ile Ser Thr Leu Ser Cys Glu Asn Lys Ile
65 70 75 80

35 Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr Lys
85 90 95

Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn Lys
100 105 110

40 Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Cys Glu
115 120 125

45 Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp Glu Leu
130 135 140

Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp
145 150 155

50 <210> 10
<211> 157
<212> PRT
<213> Unknown Organism

55 <220>
<223> Description of Unknown Organism: rodent; surmised
Mus sp.

60 <400> 10
Glu Lys Glu Leu Arg Ala Ala Ser Pro Ser Leu Arg His Val Gln Asp

	Thr 145	Cys	His	Leu	His	Phe 150	Pro	Lys	Ser	Cys	Val 155	Leu	Gly	Pro	Ile	Lys 160	
5	tgg Trp	tat Tyr	aag Lys	gac Asp	tgt Cys 165	aac Asn	gag Glu	att Ile	aaa Lys	ggg Gly 170	gag Glu	cgg Arg	ttc Phe	act Thr	gtt Val 175	ttg Leu	528
10	gaa Glu	acc Thr	agg Arg	ctt Leu 180	ttg Leu	gtg Val	agc Ser	aat Asn	gtc Val 185	tcg Ser	gca Ala	gag Glu	gac Asp	aga Arg	ggg Gly	aac Asn	576
15	tac Tyr	gcg Ala	tgt Cys 195	caa Gln	gcc Ala	ata Ile	ctg Leu	aca Thr	cac His	tca Ser	ggg Gly	aag Lys	cag Gln	tac Tyr	gag Glu	gtt Val	624
20	tta Leu	aat Asn 210	ggc Gly	atc Ile	act Thr	gtg Val	agc Ser	att Ile	aca Thr	gaa Glu	aga Arg	gct Ala	gga Gly	tat Tyr	gga Gly	gga Gly	672
25	agt Ser 225	gtc Val	cct Pro	aaa Lys	atc Ile	att Ile	tat Tyr	cca Pro	aaa Lys	aat Asn	cat His	tca Ser	att Ile	gaa Glu	gta Val	cag Gln 240	720
30	ctt Leu	ggt Gly	acc Thr	act Thr	ctg Leu 245	att Ile	gtg Val	gac Asp	tgc Cys	aat Asn	gta Val	aca Thr	gac Asp	acc Thr	aag Lys	gat Asp 255	768
35	aat Asn	aca Thr	aat Asn	cta Leu	cga Arg	tgc Cys	tgg Trp	aga Arg	gtc Val	aat Asn	aac Asn	act Thr	ttg Leu	gtg Val	gat Asp	gat Asp	816
40	tac Tyr	tat Tyr	gat Asp 275	gaa Glu	tcc Ser	aaa Lys	cga Arg	atc Ile	aga Arg	gaa Glu	ggg Gly	gtg Val	gaa Glu	acc Thr	cat His	gtc Val	864
45	tct Ser	ttt Phe 290	cgg Arg	gaa Glu	cat His	aat Asn	ttg Leu	tac Tyr	aca Thr	gta Val	aac Asn	atc Ile	acc Thr	ttc Phe	ttg Leu	gaa Glu	912
50	gtg Val 305	aaa Lys	atg Met	gaa Glu	gat Asp	tat Tyr	ggc Gly	ctt Leu	cct Pro	ttc Phe	atg Met	tgc Cys	cac His	gct Ala	gga Gly	gtg Val 320	960
55	tcc Ser	aca Thr	gca Ala	tac Tyr	att Ile	ata Ile	tta Leu	cag Gln	ctc Leu	cca Pro	gct Ala	ccg Pro	gat Asp	ttt Phe	cga Arg	gct Ala	1008
60	tac Tyr	ttg Leu	ata Ile	gga Gly	ggg Gly	ctt Leu	atc Ile	gcc Ala	ttg Leu	gtg Val	gct Ala	gtg Val	gct Ala	gtg Val	tct Ser	gtt Val	1056
65	gtg Val	tac Tyr	ata Ile	tac Tyr	aac Asn	att Ile	ttt Phe	aag Lys	atc Ile	gac Asp	att Ile	gtt Val	ctt Leu	tgg Trp	tat Tyr	cga Arg	1104
70	agt Ser	gcc Ala	ttc Phe	cat His	tct Ser	aca Thr	gag Glu	acc Thr	ata Ile	gta Val	gat Asp	ggg Gly	aag Lys	ctg Leu	tat Tyr	gac Asp	1152
75	gcc Ala	tat Tyr	gtc Val	tta Leu	tac Tyr	ccc Pro	aag Lys	ccc Pro	cac His	aag Lys	gaa Glu	agc Ser	cag Gln	agg Arg	cat His	gcc Ala	1200

1040094500

```

385          390          395          400
gtg gat gcc ctg gtg ttg aat atc ctg ccc gag gtg ttg gag aga caa 1248
Val Asp Ala Leu Val Leu Asn Ile Leu Pro Glu Val Leu Glu Arg Gln
5          405          410          415

tgt gga tat aag ttg ttt ata ttc ggc aga gat gaa ttc cct gga caa 1296
Cys Gly Tyr Lys Leu Phe Ile Phe Gly Arg Asp Glu Phe Pro Gly Gln
          420          425          430

10 gcc gtg gcc aat gtc atc gat gaa aac gtt aag ctg tgc agg agg ctg 1344
Ala Val Ala Asn Val Ile Asp Glu Asn Val Lys Leu Cys Arg Arg Leu
          435          440          445

15 att gtc att gtg gtc ccc gaa tcg ctg ggc ttt ggc ctg ttg aag aac 1392
Ile Val Ile Val Val Pro Glu Ser Leu Gly Phe Gly Leu Leu Lys Asn
          450          455          460

20 ctg tca gaa gaa caa atc gcg gtc tac agt gcc ctg atc cag gac ggg 1440
Leu Ser Glu Glu Gln Ile Ala Val Tyr Ser Ala Leu Ile Gln Asp Gly
          465          470          475          480

atg aag gtt att ctc att gag ctg gag aaa atc gag gac tac aca gtc 1488
Met Lys Val Ile Leu Ile Glu Leu Glu Lys Ile Glu Asp Tyr Thr Val
25          485          490          495

atg cca gag tca att cag tac atc aaa cag aag cat ggt gcc atc cgg 1536
Met Pro Glu Ser Ile Gln Tyr Ile Lys Gln Lys His Gly Ala Ile Arg
          500          505          510

30 tgg cat ggg gac ttc acg gag cag tca cag tgt atg aag acc aag ttt 1584
Trp His Gly Asp Phe Thr Glu Gln Ser Gln Cys Met Lys Thr Lys Phe
          515          520          525

35 tgg aag aca gtg aga tac cac atg ccg ccc aga agg tgt cgg ccg ttt 1632
Trp Lys Thr Val Arg Tyr His Met Pro Pro Arg Arg Cys Arg Pro Phe
          530          535          540

40 ctc cgg tcc acg tgc cgc agc aca cac ctc tgt acc gca ccg cag gcc 1680
Leu Arg Ser Thr Cys Arg Ser Thr His Leu Cys Thr Ala Pro Gln Ala
          545          550          555          560

cag aac tag 1689
45 Gln Asn

<210> 13
<211> 562
<212> PRT
50 <213> Unknown Organism
    <223> Description of Unknown Organism: primate; surmised
        Homo sapiens

<400> 13
55 Met Trp Ser Leu Leu Leu Cys Gly Leu Ser Ile Ala Leu Pro Leu Ser
    1          5          10          15

Val Thr Ala Asp Gly Cys Lys Asp Ile Phe Met Lys Asn Glu Ile Leu
          20          25          30

60 Ser Ala Ser Gln Pro Phe Ala Phe Asn Cys Thr Phe Pro Pro Ile Thr

```

	35	40	45
	Ser Gly Glu Val Ser Val Thr Trp Tyr Lys Asn Ser Ser Lys Ile Pro		
5	50	55	60
	Val Ser Lys Ile Ile Gln Ser Arg Ile His Gln Asp Glu Thr Trp Ile		
	65	70	75
10	Leu Phe Leu Pro Met Glu Trp Gly Asp Ser Gly Val Tyr Gln Cys Val		
	85	90	95
	Ile Lys Gly Arg Asp Ser Cys His Arg Ile His Val Asn Leu Thr Val		
	100	105	110
15	Phe Glu Lys His Trp Cys Asp Thr Ser Ile Gly Gly Leu Pro Asn Leu		
	115	120	125
	Ser Asp Glu Tyr Lys Gln Ile Leu His Leu Gly Lys Asp Asp Ser Leu		
20	130	135	140
	Thr Cys His Leu His Phe Pro Lys Ser Cys Val Leu Gly Pro Ile Lys		
	145	150	155
25	Trp Tyr Lys Asp Cys Asn Glu Ile Lys Gly Glu Arg Phe Thr Val Leu		
	165	170	175
	Glu Thr Arg Leu Leu Val Ser Asn Val Ser Ala Glu Asp Arg Gly Asn		
	180	185	190
30	Tyr Ala Cys Gln Ala Ile Leu Thr His Ser Gly Lys Gln Tyr Glu Val		
	195	200	205
	Leu Asn Gly Ile Thr Val Ser Ile Thr Glu Arg Ala Gly Tyr Gly Gly		
35	210	215	220
	Ser Val Pro Lys Ile Ile Tyr Pro Lys Asn His Ser Ile Glu Val Gln		
	225	230	235
40	Leu Gly Thr Thr Leu Ile Val Asp Cys Asn Val Thr Asp Thr Lys Asp		
	245	250	255
	Asn Thr Asn Leu Arg Cys Trp Arg Val Asn Asn Thr Leu Val Asp Asp		
	260	265	270
45	Tyr Tyr Asp Glu Ser Lys Arg Ile Arg Glu Gly Val Glu Thr His Val		
	275	280	285
	Ser Phe Arg Glu His Asn Leu Tyr Thr Val Asn Ile Thr Phe Leu Glu		
50	290	295	300
	Val Lys Met Glu Asp Tyr Gly Leu Pro Phe Met Cys His Ala Gly Val		
	305	310	315
55	Ser Thr Ala Tyr Ile Ile Leu Gln Leu Pro Ala Pro Asp Phe Arg Ala		
	325	330	335
	Tyr Leu Ile Gly Gly Leu Ile Ala Leu Val Ala Val Ala Val Ser Val		
	340	345	350
60	Val Tyr Ile Tyr Asn Ile Phe Lys Ile Asp Ile Val Leu Trp Tyr Arg		
	355	360	365

0075045 00404

	Ser	Ala	Phe	His	Ser	Thr	Glu	Thr	Ile	Val	Asp	Gly	Lys	Leu	Tyr	Asp	
	370						375					380					
5	Ala	Tyr	Val	Leu	Tyr	Pro	Lys	Pro	His	Lys	Glu	Ser	Gln	Arg	His	Ala	
	385					390					395					400	
	Val	Asp	Ala	Leu	Val	Leu	Asn	Ile	Leu	Pro	Glu	Val	Leu	Glu	Arg	Gln	
				405						410					415		
10	Cys	Gly	Tyr	Lys	Leu	Phe	Ile	Phe	Gly	Arg	Asp	Glu	Phe	Pro	Gly	Gln	
				420					425					430			
	Ala	Val	Ala	Asn	Val	Ile	Asp	Glu	Asn	Val	Lys	Leu	Cys	Arg	Arg	Leu	
15			435				440						445				
	Ile	Val	Ile	Val	Val	Pro	Glu	Ser	Leu	Gly	Phe	Gly	Leu	Leu	Lys	Asn	
	450					455						460					
20	Leu	Ser	Glu	Glu	Gln	Ile	Ala	Val	Tyr	Ser	Ala	Leu	Ile	Gln	Asp	Gly	
	465					470					475					480	
	Met	Lys	Val	Ile	Leu	Ile	Glu	Leu	Glu	Lys	Ile	Glu	Asp	Tyr	Thr	Val	
				485						490					495		
25	Met	Pro	Glu	Ser	Ile	Gln	Tyr	Ile	Lys	Gln	Lys	His	Gly	Ala	Ile	Arg	
				500					505					510			
	Trp	His	Gly	Asp	Phe	Thr	Glu	Gln	Ser	Gln	Cys	Met	Lys	Thr	Lys	Phe	
30			515					520					525				
	Trp	Lys	Thr	Val	Arg	Tyr	His	Met	Pro	Pro	Arg	Arg	Cys	Arg	Pro	Phe	
		530					535					540					
35	Leu	Arg	Ser	Thr	Cys	Arg	Ser	Thr	His	Leu	Cys	Thr	Ala	Pro	Gln	Ala	
	545					550					555					560	
	Gln	Asn															
40																	
	<210>	14															
	<211>	1686															
45	<212>	DNA															
	<213>	Unknown Organism															
	<220>																
50	<223>	Description of Unknown Organism: rodent; surmised															
		Rattus sp.															
	<220>																
	<221>	CDS															
	<222>	(1)..(1683)															
55	<400>	14															
	atg	ggg	atg	cca	ccc	ttg	ctc	ttc	tgt	tgg	gtg	tct	ttc	gtg	ctt	cca	48
	Met	Gly	Met	Pro	Pro	Leu	Leu	Phe	Cys	Trp	Val	Ser	Phe	Val	Leu	Pro	
	1				5					10					15		
60	ctt	ttt	gtg	gca	gca	ggt	aac	tgt	act	gat	gtc	tat	atg	cac	cat	gag	96

[illegible]

270

[illegible]

	gcc atc cag tgg gat ggg gac ttc aca gag cag gca cag tgc gcc aag	1584
	Ala Ile Gln Trp Asp Gly Asp Phe Thr Glu Gln Ala Gln Cys Ala Lys	
	515 520 525	
5	acg aaa ttc tgg aag aaa gtg aga tat cat atg cca ccc agg agg tac	1632
	Thr Lys Phe Trp Lys Lys Val Arg Tyr His Met Pro Pro Arg Arg Tyr	
	530 535 540	
10	ccg gca tct ccc ccc gtc cag ctg cta gga cac aca ccc cgc ata cca	1680
	Pro Ala Ser Pro Pro Val Gln Leu Leu Gly His Thr Pro Arg Ile Pro	
	545 550 555 560	
15	ggc tag	1686
	Gly	
	<210> 15	
	<211> 561	
20	<212> PRT	
	<213> Unknown Organism	
	<223> Description of Unknown Organism: rodent; surmised	
	Mus sp.	
25	<400> 15	
	Met Gly Met Pro Pro Leu Leu Phe Cys Trp Val Ser Phe Val Leu Pro	
	1 5 10 15	
30	Leu Phe Val Ala Ala Gly Asn Cys Thr Asp Val Tyr Met His His Glu	
	20 25 30	
	Met Ile Ser Glu Gly Gln Pro Phe Pro Phe Asn Cys Thr Tyr Pro Pro	
	35 40 45	
35	Val Thr Asn Gly Ala Val Asn Leu Thr Trp His Arg Thr Pro Ser Lys	
	50 55 60	
	Ser Pro Ile Ser Ile Asn Arg His Val Arg Ile His Gln Asp Gln Ser	
40	65 70 75 80	
	Trp Ile Leu Phe Leu Pro Leu Ala Leu Glu Asp Ser Gly Ile Tyr Gln	
	85 90 95	
45	Cys Val Ile Lys Asp Ala His Ser Cys Tyr Arg Ile Ala Ile Asn Leu	
	100 105 110	
	Thr Val Phe Arg Lys His Trp Cys Asp Ser Ser Asn Glu Glu Ser Ser	
	115 120 125	
50	Ile Asn Ser Ser Asp Glu Tyr Gln Gln Trp Leu Pro Ile Gly Lys Ser	
	130 135 140	
	Gly Ser Leu Thr Cys His Leu Tyr Phe Pro Glu Ser Cys Val Leu Asp	
55	145 150 155 160	
	Ser Ile Lys Trp Tyr Lys Gly Cys Glu Glu Ile Lys Val Ser Lys Lys	
	165 170 175	
60	Phe Cys Pro Thr Gly Thr Lys Leu Leu Val Asn Asn Ile Asp Val Glu	
	180 185 190	

	Asp	Ser	Gly	Ser	Tyr	Ala	Cys	Ser	Ala	Arg	Leu	Thr	His	Leu	Gly	Arg
	195							200					205			
5	Ile	Phe	Thr	Val	Arg	Asn	Tyr	Ile	Ala	Val	Asn	Thr	Lys	Glu	Val	Gly
	210						215					220				
	Ser	Gly	Gly	Arg	Ile	Pro	Asn	Ile	Thr	Tyr	Pro	Lys	Asn	Asn	Ser	Ile
	225					230					235					240
10	Glu	Val	Gln	Leu	Gly	Ser	Thr	Leu	Ile	Val	Asp	Cys	Asn	Ile	Thr	Asp
					245					250					255	
	Thr	Lys	Glu	Asn	Thr	Asn	Leu	Arg	Cys	Trp	Arg	Val	Asn	Asn	Thr	Leu
				260					265					270		
15	Val	Asp	Asp	Tyr	Tyr	Asn	Asp	Phe	Lys	Arg	Ile	Gln	Glu	Gly	Ile	Glu
			275					280					285			
	Thr	Asn	Leu	Ser	Leu	Arg	Asn	His	Ile	Leu	Tyr	Thr	Val	Asn	Ile	Thr
20		290					295					300				
	Phe	Leu	Glu	Val	Lys	Met	Glu	Asp	Tyr	Gly	His	Pro	Phe	Thr	Cys	His
	305					310					315					320
25	Ala	Ala	Val	Ser	Ala	Ala	Tyr	Ile	Ile	Leu	Lys	Arg	Pro	Ala	Pro	Asp
					325					330					335	
	Phe	Arg	Ala	Tyr	Leu	Ile	Gly	Gly	Leu	Met	Ala	Phe	Leu	Leu	Leu	Ala
				340					345					350		
30	Val	Ser	Ile	Leu	Tyr	Ile	Tyr	Asn	Thr	Phe	Lys	Val	Asp	Ile	Val	Leu
			355					360					365			
	Trp	Tyr	Arg	Ser	Thr	Phe	His	Thr	Ala	Gln	Ala	Pro	Asp	Asp	Glu	Lys
35		370					375					380				
	Leu	Tyr	Asp	Ala	Tyr	Val	Leu	Tyr	Pro	Lys	Tyr	Pro	Arg	Glu	Ser	Gln
	385					390					395					400
40	Gly	His	Asp	Val	Asp	Thr	Leu	Val	Leu	Lys	Ile	Leu	Pro	Glu	Val	Leu
					405					410					415	
	Glu	Lys	Gln	Cys	Gly	Tyr	Lys	Leu	Phe	Ile	Phe	Gly	Arg	Asp	Glu	Phe
				420					425					430		
45	Pro	Gly	Gln	Ala	Val	Ala	Ser	Val	Ile	Asp	Glu	Asn	Ile	Lys	Leu	Cys
			435					440					445			
	Arg	Arg	Leu	Met	Val	Leu	Val	Ala	Pro	Glu	Thr	Ser	Ser	Phe	Ser	Phe
50		450					455					460				
	Leu	Lys	Asn	Leu	Thr	Glu	Glu	Gln	Ile	Ala	Val	Tyr	Asn	Ala	Leu	Val
	465					470					475					480
55	Gln	Asp	Gly	Met	Lys	Val	Ile	Leu	Ile	Glu	Leu	Glu	Arg	Val	Lys	Asp
					485					490					495	
	Tyr	Ser	Thr	Met	Pro	Glu	Ser	Ile	Gln	Tyr	Ile	Arg	Gln	Lys	His	Gly
				500					505					510		
60	Ala	Ile	Gln	Trp	Asp	Gly	Asp	Phe	Thr	Glu	Gln	Ala	Gln	Cys	Al	

DX01073K

525

5

10

Gly

	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2
--	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	---